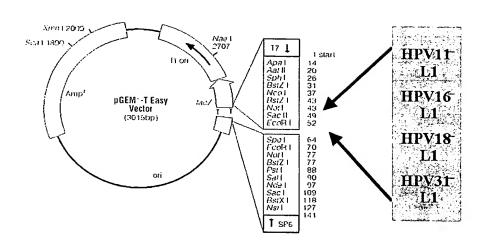
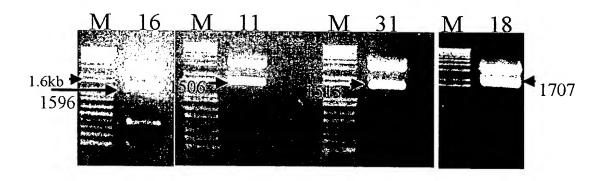
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Fig. 1





**(B)** 



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	1	10	20	30	40	50	60	70	80	90	100	110	120	130
RF402678 HPV16 Consensus	HILL	LIGHT OF LIFE	INTRINCHI	J. 11651 1811 18	0.81611813	HHHHT GHT GT	RARCGITTAC	CATATITITI	TTCRGATGTC TTCRGATGTC TTCRGATGTC	TOTTTOCOTO	CCTOCTCOCC	CCOCTCTCTO	CTICCCICCIC	TCCCC
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
AF402678 HPV16 Consensus								CATCCAGACT	ACTTGCRGTTI ACTTGCRGTTI ACTTGCRGTTI	GREATECET	RTTTTCCTAT	TARARA-CCT	RRCAN TRACAF RACAN TAACAF	RATATT RATATT
RF402678	1							330	340	350	360	370	380	390
HPV16 Consensus									CCTGRERECTI CCTGRERECTI CCTGRERECTI					
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
RF 402678 HPV16 Consensus									CRGARARTGC CRGARARTGC CRGARRATGC					
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
RF 402678 HPV16 Consensus	CTATE								ATCCCCATGTI ATCCCCATGTI ATCCCCATGTI					
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
RF402678 HPV16 Consensus									AACARRAGTGI AACARRAGTGI AACARRAGTGI					
	781	790	800	810	620	830	840	850	860	870	880	890	900	910
RF402678 HPV16 Consensus									ATTTATTTRA ATTTATTTRA ATTTATTTRA					
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
RF402678 HPV16 Consensus		TCTGGGTC							TGATGCCCRAS TGATGCCCRAS TGATGCCCRAS		RECTIBITE	GTTACAACGA GTTACAACGA	GCRCRGGGCCF GCRCRGGGCCF	CAATAA Caataa
RF 402678	1								GCTGCCATATI		1140	1150	1160	1170
HPV16 Consensus	TGGCA	TTTGTTGG	G TAACCARC T						ec teccutate ec teccutate					
	1171		1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
									CRTACATRON CRTACATRON CRTACATRON					
	1301	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
									RCCTCCRGCRC RCCTCCRGCRC RCCTCCRGCRC					
	1431	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560
									GCCARRCCAR GCCARRCCAR GCCRARCCAR					
RF402678 HPV16 Consensus	TETRO	RACTGCTA	1580 IRCGCRARRAR IRCGCRARRAR	CGTRAGCTG										

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	1	10	20	30	40	50	60	70	80	90	100	110	120	130
J04353 HPV31_L1 Consonsus								TGTRAGEREGG TGTRAGEREGG TGTRAGEREGG						TGCTTA
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
J04353 HPV31_L1 Consensus	CRGTI CRGTI CRGTI	RGGCCATCO RGGCCATCO RGGCCATCO	ATATIATICCE ATATIATICCE ATATIATICCE	TRCCTRARTO TRCCTARRTO TRCCTARRTO	TGACRATCO TGACRATCO TGACRATCO	TARRAGAATR TARRAGAATR TARRAGAATR	GTTGTACCE GTTGTACCE GTTGTACCE	RRGGTGTCAGG RRGGTGTCAGG	ATTRCARTAT ATTRCARTAT ATTRCARTAT	RGGGTATTTA RGGGTATTTA RGGGTATTTA	GGTTCGTTT GGGTTCGTTTT	RCCRGATCCRI RCCRGATCCRI RCCRGATCCRI	RACAMETTTGE RACAMETTTGE RACAMETTTGE	ATTICC ATTICC ATTICC
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
J04353 HPV31_11 Consensus								TRGGTCGCGGG TRGGTCGCGGG TRGGTCGCGGG						
	391	400	410	420	430	440	450	460	470	490	490	500	510	520
J04353 HPV31_L1 Consensus	GARRE	RETETRATA	GATATECCEGT GATATECCEGT GATATECCEGT	GGTCCTGGCI GGTCCTGGCI GGTCCTGGCI	CTGATAATA CTGATAATA CTGATAATA	GGGARTGTAT GGGARTGTAT GGGARTGTAT	ATCARTGGE ATCARTGGE ATCARTGGE	TTATRAACAAR TTATRAACAAR TTATRAACAAR	CRCRACTGTG CRCRACTGTG CRCRRCTGTG	TTRCTTGGT TTRCTTGGT TTRCTTGGT	TGCRRRCCRC TGCRRRCCRC TGCRRRCCRC	TATTGGAGA TATTGGAGA TATTGGAGA	SCATTGGGGTF SCATTGGGGTF SCATTGGGGTF	IRRGGTR IRRGGTR IRRGGTR
	521	530	540	550	560	570	580	590	600	610	620	630	E40	650
J04353 EPV31_L1 Consensus	GTCCT	TETRETRA	CRATECTATTA CRATECTATTA CAATECTATTA	CCCCTGGTGG CCCCTGGTGG CCCCTGGTGG		ATTREARTTR ATTREARTTR ATTREARTTR	ARRENTTCE BARRENTTCE BARRENTTCE	GTTATACANGA GTTATAGANGA GTTATACANGA	TGGGGATATG TGGGGATATG TGGGGATATG	STERTACRES STERTACRES STERTACRES	GCTTTGGRGC GCTTTGGRGC GCTTTGGRGC	TATGGATTTT TATGGATTTT TATGGATTTT	RCTGCTTTRCF RCTGCTTTRCF RCTGCTTTRCF	AGACAC AGACAC AGACAC
	651 	660	670	680	690	700	710	720	730	740	750	760	770	780
J04353 HPV31_1.1 Consensus	TRARE TRARE	RGTRATGTT RGTRATGTT RGTRATGTT	CCTTTGGACAT CCTTTGGACAT CCTTTGGACAT	TTGTAATTC TTGTAATTC TTGTAATTC	TATTTGTRAA TATTTGTRAA TATTTGTRAA	TATCCAGATTI TATCCAGATTI TATCCAGATTI	ATCTTRARA ATCTTRARA ATCTTRARA	TGGTTGCTGRG TGGTTGCTGRG TGGTTGCTGRG	CCATATGGCG CCATATGGCG CCATATGGCG	TRCATTATT TRCATTATT TRCATTATT	TTTTATTR TTTTATTR TTTTATTR	GTAGGGAACI GTAGGGAACI GTAGGGAACI	RARTGITIGTE BARTGITIGTE BARTGITTGTE	IAGGCAT IRGGCAT IAGGCAT
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
J04353 HPV31_L1 Consensus		TRATAGAT TRATAGAT TRATAGAT	CAGGCACGGTT CAGGCACGGTT CAGGCACGGTT	GGTGARTCGG GGTGARTCGG GGTGARTCGG	TECCTACTS TECCTACTS TECCTACTS	ACTTATATAT ACTTATATAT ACTTATATAT	TARRESCTO TARRESCTO TARRESCTO	CGGTTCRACAS CGGTTCRACAS CGGTTCRACAS	CTRCTTTRGC CTRCTTTRGC CTRCTTTRGC	RACAGTACA TRACAGTACA TRACAGTACA	TRCTTTCCTAL TRCTTTCCTAL TRCTTTCCTAL	ACC TAGCGGI ACC TAGCGGI ACC TAGCGGI	TCCATGGTTE TCCATGGTTE TCCATGGTTE	CTTCAG ICTTCAG ICTTCAG
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
J04353 HPV31_L1 Consensus	ATGCF ATGCF	CARATTII CARATTII	TRATRARCCRT TRATRARCCRT TRATRARCCRT	ATTGGATGCE ATTGGATGCE ATTGGATGCE	RACGTGCTCA RACGTGCTCA RACGTGCTCA	GGGRERERATI GGGRERERATI GGGRERERATI	RATEGTATT RATEGTATT RATEGTATT	TETTGGGGCRR TETTGGGGCRR TETTGGGGCRR	TCAGTTATTT TCAGTTATTT TCAGTTATTT	TTACTGTGG TTACTGTGG	TREATRICACI TREATRICACI TREATRICACI	CGTRGTACCI CGTRGTACCI CGTRGTACCI	ATATGTCT61 ATATGTCT61 ATATGTCT61	TIGIGE TIGIGE TIGIGE
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
J04353 HPV31_L1 Consensus								GTGAGGAATTT GTGAGGAATTT GTGAGGAATTT						
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1290	1290	1300
J04353 HPV31_L1 Consensus								CTCRGGTTCTT CTCRGGTTCTT CTCRGGTTCTT						
	1	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
J04353 HPV31_11 Consensus								ARSTTTTCTGC BRGTTTTCTGC BRGTTTTCTGC						
	1431	1440	1450	1460	1470	1490	1490	1500	151812					
J04353 HPV31_L1 Consensus	HUBIL	лифии	HOHOLLINGS I FIR	REGIRATECA	RLLCALBELD.	TOTROPORTOR	<b>OCTOCTOO</b>	RRCGTARAARA RRCGTARAARA RRCGTARAARA	200000720					

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	1 10	20	30	40	50	60	70	80	90	100	110	120	130
MC_001525 HPV11_L1 Consensus	ATETGECGCCT ATETGECGCCT ATETGECGCCT	H14L15H1.H04LH03	<b>B</b> GTHI ATGTG	CETELLECEN	SCCC TELETC	CRRCETTET	TECCENCENTE	nctorettee	DCCCDCC DOC	OTOTYYPIC	TOCOCCOC	FICTOCOCTO	OTTOOTE.
	131 140	150	160	170	180	190	200	210	220	230	240	250	260
MC_001525 MPV11_L1 Consensus	TGGGRCATCCAT TGGGRCATCCAT TGGGRCATCCAT												
	261 270	280	290	300	310	320	330	340	350	360	370	380	390
MC_001525 HPV11_L1 Consensus	GTTTGRCCCCAC GTTTGRCCCCAC GTTTGRCCCCAC												
	391 400	410	420	430	440	450	460	470	490	430	500	510	520
HPV11_L1 Consensus	GGGTATGGTGGT GGGTATGGTGGT GGGTATGGTGGT												
	521 530	540	550	560	570	580	590	600	610	620	630	640	650
NC_001525 HPV11_L1 Consensus	ATRECTETGTRES ATRECTETGTRES ATRECTETGTRES	RRARTGGTGACT	GCCCCCCGT	TGGRACTTAT									
	651 660	670	680	690	700	710	720	730	740	750	760	770	780
HC_001525 HPV11_L1 Consensus	TECCETTGATAT TECCETTGATAT TECCETTGATAT												
	781 790	800	B10	820	830	840	850	860	870	880	690	900	910
MC_001525 HPV11_11 Consensus	GCCGGTRCTGTG GCCGGTRCTGTG GCCGGTRCTGTG												
	911 920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
MC_001525 HPV11_L1 Consensus	TTAATARRCCATI TTAATARRCCATI TTAATARRCCATI												
	1041 1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1150	1170
HC_001525 HPV11_L1 Consensus	ATCTGCTRCATR RTCTGCTRCATR ATCTGCTACATR												
	1171 1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
MC_001525 HPV11_L1 Consensus	RATCCTTCTGTT RATCCTTCTGTT												
	1301 1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430
MC_001525 HPV11_L1 Consensus	RGGATCCCTATA RGGATCCCTATA RGGATCCCTATA												
	1431 1440	1450	1460	1470	1490	1490	1508503						
NC_001525 HPV11_L1 Consensus	TACAGGTATARA TACAGGTATARA TACAGGTATARA	SCGCCCAGCTGT	GTCTRRGCC	CTCTACRECCC	CCARRCGRA	RREGIRECTRE	BRRCCBRRRRR						

NC 001357	1	10	20	30	40	50		70	80	50	100	110	120	130
HPV1BL1-U HPV1BL1-L Consensus					THE CHIEF THE	CICCICIOIN	IUGELECTIO	Inicaccent	HULLUL I ULL	I CHICHCHGI	HIRITGGTAT	ACATEGTACI	RCATTATTATT RCATTATTATT RCATTATTATT	TGTGGCC
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
NC_001357 HPV18L1-U HPV18L1-L				KO 1120KU	di icce ini	111111GLINGS	RIGGLIIIGI	WILLIAM I HIS	TGRCRATACC TGRCRATACC	GTATATETTE GTATATETTE	CACCICCTIC	TGTGGCRAG	RETTETRASTA RETTETRASTA	CCGATGA CCGATGA
Consensus								GGCGGCCTRG	TGACRATACC	GTATATETTC	CACCTCCTTC	TETEGCARG	RGTTGTARRTR	CCGATGA
	261 1	270	280	290	300	310	320	330	340	350	360	370	380	390
MC_001357 HPV18L1-U HPV18L1-L Consensus					-	CACAMIT I IS I I I INC.	CIGIIGGIAA	ICCN INT I I I	H000011LLIU	LXU6   66   66	CHA TANGCAG	GA TAT TCCTS	RAGGTTTCTGC RAGGTTTCTGC	ATRCCAA
	391	400	<b>4</b> 10	420	430	440	#50	450	470					
NC_001357	TRIBG	AGTATTIRGE	SETECRETTER	CTERCCOR	OTDOGTTTC	CTTTOCCTCOT				460	490	500	510 TEGCCETGET	520
HPV18L1-U HPV18L1-L Consensus						or rince runs	incinaini i	INIMITTIE	<b>WINTHUMEN</b>	11118616166	eccielecie	GRIGT GGRRRIT	TEGCCETEST: TEGCCETEST: TEGCCETEST	CAGCCTT
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
NC_001357	TREGT	GTTGGCCTT	RGTGGGCRTCC	ATTTTATAR	TARATTAGA	TGACACTGARA	GTTCCCATG	CCGCCRCGTC	TRATETITET				TATARGERGA	
HPV18L1-U HPV18L1-L Consensus			RG TGGGCATCC RG TGGGCATCC			TOTAL TOTAL	direcenta	CCUCCHCUIC	INDIGITIES.	CHPPRICE LIH	Li	arc rormon	miniochon	LINCHELL
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
NC_001357 HPV18L1-U HPV18L1-L Consensus	ATGTA	TTTTGGGCTG	TGCCCCTGCT	HTTGGGGRA	CACTGGGCTI	RANGGERETGE	TTSTRATE	SCGTCCTTTR	TCRCRGGGG	ATTGCCCCCC	TTTAGAACTTA	MANAGERE	STTTTGGRAGA	TGGTGAT
	781	790	800	B10	820	830	840	850	860	870	880	890	900	910
MC_001357 HPV18L1-U HPV18L1-L Consensus					o inchi idei	unon i nu i nere	i i G i Grago i M	CCRITOGRIN	HIGICIGAL	THTTTTHAN	TATCCTGATTA	TTTACAAAT	GTCTGCRGATI	CCTTATG
	911	320	930	940	950	960	970	990	990	1000	4040			
NC_001357	1				-		970	980	990	1000	1010	1020	1030	1040
NC_001357 HPV18L1-U HPV18L1-L Consensus	GGGAT	TCCATGTTT	TTTGCTTRCG	GCGTGAGCA	ecrimeci	TREGENTTTTT	GGARTAGAG	CRESTRETATI	SEGTENCRET	STGCCTCART		1020 RANGGERER	1030 IGGTATGCCTG	
HPV18L1-U HPV18L1-L Consensus	1041	TCCATGTTT	1060	GCSTGAGCA	1080	INGGCRITITI	GGARTAGAG	CRGGTACTATO	1120	TGCCTCRRT	CCTTRTATATI	TRANGGCACA	1150	TTCRCC
HPV18L1=U HPV18L1=L	1041 TGGCRI	1050 SCTGTGTGTG	1060	GCGTGAGCA 1070 CCARGTGGC	1080	INGGCRITITI	GGARTAGAG	CRGGTACTATO	1120	TGCCTCRRT	CCTTRTATATI	TRANGGCACA	GETATECCTE	TTCRCC
HPV18L1-U HPV18L1-L Consensus NC_001357 HPV18L1-U HPV18L1-L Consensus	1041 TGGCRI	1050 SCIGIGIGIA 1180	1060 10711111111111111111111111111111111	1070 CCRRSTGSC	1080 TCTATTGTTE	1090 RECETETGACTE	1100 CCRGTTGTT	1110 TRATABACCET	1120 FRYTEGTYACI	1130 PTRANGGCACAN	1140 GGGTCRTARCE	1150 INTEGTETTT	1150 GCTGSCATAAT	1170 1170 TCARTTR
HPV18L1-U HPV18L1-L Consensus MC_001357 HPV18L1-U HPV18L1-L	1041 TGGCRI	1050 SCIGIGIGIA 1180	1060 10711111111111111111111111111111111	1070 CCRRSTGSC	1080 TCTATTGTTE	1090 RECETETGACTE	1100 CCRGTTGTT	1110 TRATABACCET	1120 FRYTEGTYACI	1130 PTRANGGCACAN	1140 GGGTCATAACA	1150 INTEGTETTT	1150	1170 1170 TCARTTR
HPV18L1-U HPV18L1-L Consensus MC_001357 HPV18L1-U HPV18L1-L Consensus	1041 TGGCRI	1050 SCTGTGTGTR 1180	1060 HTTETCCCTCTI 1190 IGRTACERCTC	1070 CCRRETGEC 1200 CCRETRICCR	1080 TCTATTGTTS  1210 RTTTBBCBBT	1090 ECCTCTGACTC 1220 FATGTGCTTCT	1100 CCRGTTGTT  1230 RCRCRGTCTC CRGTCTC	1110 TRATABACCAT  1240 CCTGTRCCTGC	1120 INTEGRATACI  1250 GCRATATGAT GCRATATGAT GCRATATGAT	1130  TRANGGCACAN  1260  TGCTACCARA:	1140 GOGTCATARCE  1270 TTTRRGCRGTE TTTRRGCRGTE	1150 HTGGTGTTT  1290 HTGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1150 GCTGSCATAAT	1170 1170 ICARTTA
HPV18L1-U HPV18L1-L Consensus NC_001357 HPV18L1-U HPV18L1-L Consensus NC_001357 HPV18L1-U HPV18L1-U HPV18L1-L Consensus	1041 1060AT	1050 ECTETETETE 1180 INCTETETETE	1060 1071000000000000000000000000000000000	1070 CCRRGTGGC  1200 CCRGTRCCR	1080 TCTATTGTTE  1210 RTTTBACART	1090 RECETETGACTE  1220 RATETGETTET	1100 CCRGTTGTT  1230 RCRCRGTCTC CRGTCTC 1360	1110 TRATABACCET  1240 CCTGTRCCTGC CCTGTRCCTGC	1120 TATTGGTTACI  1250 GGCRRTATGRI GGCRRTATGRI 1380	1130 BTRAGGCACAI 1260 IGCTACCARA: IGCTACCARA:	1140 55GTCRTARCE 1270 TTTRRGCRGTR TTTRRGCRGTR TTTRRGCRGTR	1150 1150 1150 1150 1150 1150 1150 1150	1160 GCTGGCHTAN1 1290 HTGTTGRGGAN1 HTGTTGRGGAN1 1420	1170 1300 1300 REGETT
HPV18L1-U HPV18L1-L Consensus MC_001357 HPV18L1-U HPV18L1-L Consensus MC_001357 HPV18L1-U HPV18L1-U	1041 1060AT 1171 1171 1171 1301 150AG	1050 1050 1180 1310	1060 HITCHCCTCT  1190 GRITACCACTCT  1320 AGGITGGGGC	1070 CCARGTGGC  1200 CCAGTACCA  1330 TATTACTTC	1080 ICTATTGTTE  1210 RTTTBACAAT  1340 RRACTGCAGAAT	1090 ECCICTGACTC 1220 FATGIFFECTICT 1350	1100 CCRGTTGTT  1230 RCRCRGCTC CRGTCTC CRGTCTT 1360 RTRITCRTRI	1110 TRATAMECCAT  1240 CETETRECTEC CETETRECTEC 1370 STATEGATTREAT	1120 IRTEGETTACI  1250 IGCRATATGA IGCRATATGA INGCRATATGA INGCRATATGA INGCRATATGA INGCRATATGA INGCRATATGA INGCRATATGA INGCRATATGA INGCRATATGA INGCRATATTIA	1130  TRANGECACH  1260  TGCTACCARA: GCTACCARA: 1390  REGATTEGA	1140 SEGETCATIANCE 1270 THERRECAGES THERRECAGES 1400 ACTITEGESTIT	1150 HTGGTGTTT  1290 HTGGGGGGGGGGTTTGGGGGGGGGGGGGGGGGGGGGGG	1160 GCTGGGATANT 1290 ITGTTGAGGANITGTTGAGGANITGTTGAGGANI 1420 CCRACTACTACT	1170 1300 TATGATT TATGATT 1430
HPV181.4-U HPV181.1-C Consensus MC_001357 HPV181.1-U HPV181.1-U Consensus MC_001357 HPV181.4-U Ensensus MC_001357 HPV181.4-U HPV181.1-U	1041 1060AT 1171 1171 1171 1301 150AG	1050 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	1060 HITCHCCTCT  1190 GRITACCACTCT  1320 AGGITGGGGC	1070 CCARGTGGC  1200 CCAGTACCA  1330 TATTACTTC	1080 ICTATTGTTE  1210 RTTTBACAAT  1340 RRACTGCAGAAT	1090 ECCICTGACTC 1220 FATGIFFECTICT 1350	1100 CCRGTTGTT  1230 RCRCRGCTC CRGTCTC CRGTCTT 1360 RTRITCRTRI	1110 TRATRANCCAT  1240 CENTRACTECTEC CENTRACTECTEC CENTRACTECTEC CENTRACTECTEC CENTRACTECTEC CENTRACTECTEC CENTRACTECTECTECTECTECTECTECTECTECTECTECTECTEC	1120 IRTISGTTACI  1250 SCORRECTES SCORRECTES SCORRECTES 1380 RECERTITIES RECERTITIES RECERTITIES	1130 PTRANGECACH  1260  1260  1260  1260  1260  1260  1390  PROGRATTGGRESSEGGATTGGATTGGATTGGATTGGATTGGATTGGATTG	1140  1270  TITRIBGERGIE  1400  ACTITIEGETETT  ACTI	1150 1150 1150 1150 1176GTGTTTT 1290 1176GGGGGGTGTTT 1176GGGGGGGGTGTTTGGGGGGGGGGGGGGGGGGGGGGG	1150 1150 1290 ITETIGAGARI 16TIGAGARI 16TIGAGARI 16TIGAGARI 1420 1CCRACTACTACTAC CCRACTACTACTACTACTACTACTACTACTACTACTACTACTA	1170  1300  TRIGATTA  1300  TRIGATT  RATGATT  RATGATT  AUGUST  TRIGAT  TRIGAT
HPY181-4 EONSENSUS  NC_001357 HPY181-1 HPY181-1 HPY181-1 HPY181-1 HPY181-1 EONSENSUS  NC_001357 HPY181-1 EONSENSUS  NC_001357 HPY181-1 HPY	10-41 1	1050 2016161616161616161616161616161616161616	1060 1060 11161CCCCTCTI 1190 GRITACCACTCC 1320 GRITAGIAC RETTGIAGIAC RETTGIAGIAC RETTGIAGIAC RETTGIAGIAC	1070 CCRRGTGGC  1200 CCRGTRCCR  1330 TRITISCITTI TRITISCITTI TRITISCITTI TRITISCITTI TRITISCITTI TRITISCITTI	1080 ICTATTGTTE  1210 RETTERCRET  1340 RRACTGCRGGT RRACTGCRGGT RRACTGCRGGT 1470	1090 SECTION S	1100 CCRGTTGTT  1230 RCRCRGTCTC CRGTCTC CRGTCTC CRGTCTC TRGTCTC TRGTCTC TRGTCTC TRGTCTC TRGTCTC TRGTCTC TRGTCTC TRGTCTC TRGTCTC TRGTCT TRGTC TRGTCT TRGTC TRGTCT TR	1110 TRATRARACCET 1240 CETETRECTES CETETRECTES CETETRECTES 1370 STATEGRATRES STATEGRATRES 13500	1120 INTEGRITACI  1250 SECRETATES SECRETATES SECRETATES SECRETATES 1380 RETATETES RETATETES 1510	1130  TRANGGENEN  1260  TGCTACCARR  TGCTACCARR  TGCTACCARR  1390  SRGGATTGGR  SRGGATTGGR  SRGGATTGGR  1520	1140  1140  1270  TITIERGERGIE  TITIERGERGIE  1400  RETITEGGET  RETITEGGET  1530	1150 HTGGTGTTT  1290 HTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1150 COTTO CONTROL CON	1170 1300 1300 1300 1316ATTA 1430 1430 14116GT
HPY181.4U EVP181.4C Consensus  NC_001357 HPY181.4U HPY181.4U HPY181.4U HPY181.4U HPY181.4L Consensus  NC_001357 HPY181.4L Consensus	1041 106681 1171 1171 1301 166861 1431 1668186	1050  1050  1180  1060  1180  1070	1060  1060  ITTECCETET  1190  IGHTACERCED  1320  RETTETETER  RETTETETER  1450  TETERETETETER	1070 CLARGIGGC  1200 CCAGIRCER  1330 INTERCTITE INTERCTITE INTERCTITE 1460 GITGCTATT	1080  TCTATTGTTE  1210  RTTTANCANT  1340  RRCTGCRGRT  RRCTGCRGRT  1470  RCCTGCRGRT	1090 SECTOTAGETECT  1220 SATERIFICATE  1250 GITHATGTCT  GITHATGTCT  1480 SAGGARGETECT	1100 CCRGTTGTT  1230 RCRCRGTCTC CRGTCTC 1360 RTRITCRTRR RTRITCRTRR RTRITCRTRR RTRITCRTRR 1490 RCCCGCTGRI	1110 1110 11110 11240 1240 1240 1240 124	1120 IRITEGITACE 1250 GCCRITATEGE GCCRITATEGE GCCRITATEGE 1380 REGIATITIES REGIATITIES REGIATITIES 1510	1130  STRANGECHCH  1260  1260  GGETHECHNIN  GGETHECHNIN	1140 SEGETCATIANCE 1270 ITTERRECEGER ITTERRECEGER ITTERRECEGER ITTERRECEGER 1400 RECTITEGER RECTITEGER 1530	1150 1150 1150 1160TETTT 1280 1176CEGERCH 1176CEGERCH 1176CEGERCH 1410 1410 1410 1410 1410 1410 1410 141	1150 1150 1290 ITETIGAGARI 16TIGAGARI 16TIGAGARI 16TIGAGARI 1420 1CCRACTACTACTAC CCRACTACTACTACTACTACTACTACTACTACTACTACTACTA	1170 ICARTIA  1300 IRIGATI
HPV181.1-U HPV181.1-U Consensus NC_001357 HPV181.1-U HPV181.1-U HPV181.1-U HPV181.1-U HPV181.1-U HPV181.1-U HPV181.1-U HPV181.1-U HPV181.1-U HPV181.1-U HPV181.1-U HPV181.1-U HPV181.1-U HPV181.1-U HPV181.1-U HPV181.1-U	1041 1066 1171 1171 1171 1301 16CR01 1431 16CR01 1431 16CR01 16CR01 16CR01 16CR01 16CR01 16CR01 16CR01 16CR01 16CR01 16CR01 16CR01	1180 1310 1718111111 1440 181111111 181111111 181111111 181111111	1060  1060  1190  1190  1320  RETIFICIENCE RETIFICIENC RETIFIC RETIFICATION RETIFICA	1070 CCRRETERC  1200 CCRRETERC  1330 TRITECTITE TRITECTIT TRITECTITE TRITECTITE TRITECTITE TRITECTITE TRITECTITE TRITECTI	1080  TOTATTGTTS  1210  RETTRACART  1340  RACTGCARGAT  RACTGCARGAT  1470  RCCTGTCARGA  RCCTGTCARGAT  1600	1090 RECEITEMENT 1220 ATERISCITET 1250 GITHARTICET 1350 REGARDETECT 1480 R	1100 CCRGTTGTT  1230 RCRGARGTCTT  1360 RTRITCRIRR RTRITCRIRR RTRITCRIRR RTRITCRIRR RTRITCRIRR RTRITCRIRR RTRITCRIRR RCGGCTGRIR RCCGGCTGRIR 1450 1450	1110 1788TARRACCRI 1240 1240 1250 1250 1370 1370 1370 1370 1370 1370 1370 137	1120 1250 1250 1250 1250 1250 1250 1250	1130 1130 1130 1130 1260 1260 1260 1260 1370 1370 1380 1380 1380 1580 1580 1580 1580 1580 1580 1580 15	1140  BEGGTERTRACE  1270  THERRECEGER  1400  BECHTEGERT  CHITEGERT  CHITEGERT  1530  THERRECEGERT  T	1150 1290 1780CRSSRCS 1780CRSSRCS 1780CRSSRCS 1780CRSSRCS 17410 1750CRSSCCS 17540 1777RASSGS 1777RASSGS 1777RASSGS	1160 1160 GCTGGCRTGAT  1290 ITCTTGGGGGAT ITCTTGGGGAT ITCTTGGGGAT ITCTTGAGGAT ITCTTGAGGAT ITCTTGAGGAT ITCTTGAGGAT ITCTTGAGGAT ITCTTGAGGAT ITCTTGAGGAT ITCTGAGGAT ITCTG	1170 1170 1170 1170 1170 1170 1170 1170
HPV181.4-U HPV181.4-L Consensus  NC_001357 HPV181.4-U HPV181.4-L Consensus  NC_001357 HPV181.4-L HPV181.4-L HPV181.4-L Consensus  NC_001357 HPV181.4-L Consensus	1041 1066 1171 1171 1171 1301 16CR01 1431 16CR01 1431 16CR01 16CR01 16CR01 16CR01 16CR01 16CR01 16CR01 16CR01 16CR01 16CR01 16CR01	1180 1310 1718111111 1440 181111111 181111111 181111111 181111111	1060  1060  1190  1190  1320  RETIFICIENCE RETIFICIENC RETIFIC RETIFICATION RETIFICA	1070 CCRRETERC  1200 CCRRETERC  1330 TRITECTITE TRITECTIT TRITECTITE TRITECTITE TRITECTITE TRITECTITE TRITECTITE TRITECTI	1080  TOTATTGTTS  1210  RETTRACART  1340  RACTGCARGAT  RACTGCARGAT  1470  RCCTGTCARGA  RCCTGTCARGAT  1600	1090 RECEITEMENT 1220 ATERISCITET 1250 GITHARTICET 1350 REGARDETECT 1480 R	1100 CCRGTTGTT  1230 RCRGARGTCTT  1360 RTRITCRIRR RTRITCRIRR RTRITCRIRR RTRITCRIRR RTRITCRIRR RTRITCRIRR RTRITCRIRR RCGGCTGRIR RCCGGCTGRIR 1450 1450	1110 1788TARRACCRI 1240 1240 1250 1250 1370 1370 1370 1370 1370 1370 1370 137	1120 1250 1250 1250 1250 1250 1250 1250	1130 1130 1130 1130 1260 1260 1260 1260 1370 1370 1380 1380 1380 1580 1580 1580 1580 1580 1580 1580 15	1140  BEGGTERTRACE  1270  THERRECEGER  1400  BECHTEGERT  CHITEGERT  CHITEGERT  1530  THERRECEGERT  T	1150 1290 1780CRSSRCS 1780CRSSRCS 1780CRSSRCS 1780CRSSRCS 17410 1750CRSSCCS 17540 1777RASSGS 1777RASSGS 1777RASSGS	1160 1160 GCTGGCRTGAT  1290 ITCTTGGGGGAT ITCTTGGGGAT ITCTTGGGGAT ITCTTGAGGAT ITCTTGAGGAT ITCTTGAGGAT ITCTTGAGGAT ITCTTGAGGAT ITCTTGAGGAT ITCTTGAGGAT ITCTGAGGAT ITCTG	1170 1170 1170 1170 1170 1170 1170 1170
HPV181.1-U HPV181.2-L Consensus  NC_001357 HPV161.1-U HPV181.1-L Consensus  NC_001357 HPV181.1-U EONSENSUS  NC_001357 HPV181.1-U EONSENSUS  NC_001357 HPV181.1-U EONSENSUS  NC_001357 HPV181.1-U EONSENSUS  NC_001357 HPV181.1-U HPV181.1-U	1041 166CRI 1171 1301 15CRG 15CRG 1431 6GATRI 15GATRI	1050  2016161616  1180  1310  118111111  118111111  1440  1440  1440  1441  14	1060 1060 11190 1190 1320 1320 1450 1450 16TREASTER 16TREASTER 16TREASTER 16TREASTER 16TREASTER 16TREASTER 16TREASTER 16TREASTER 1580 LITEGRATER	1070 CURRETGEC  1200 CURRETGEC  1200 CURRETGEC  1330 INTERCTIF INT	1080 TCTATTGTTE  1210 RTTTRACART  1340 RRCTGCRGAT RRCTGCRGAT 1470 ACCTGTCRGAT 1470 1500 TTCRGCTGCRGAT	1090  1220  ATETOCTIC  1350  GUARANTECT  GUARANTECT  1480  MAGGATECT  1510  ATTECCTCC  ATTECCTCC	1100 1230 REGERTAGE CRETCH CRETCH CRETCH TARTICETER ATRITICETER AT	1110 1240 1240 1240 1240 1240 1240 1240	1120 1250 1250 1250 1250 1250 1250 1250	1130 1260 1260 1260 1260 1260 1260 1260 1360 1360 1380 1380 1380 1520 1520 1571 1671 1671 1671 1671 1671 1671 1671	1140 1270 111496CRGTRATAGER 1270 111496CRGTRATAGER 111486CRGTRATTTRAGERGER 1400 1400 1401 1530 1530 156GRATTGER 1156GRATTGER 1156GRATTG	1150 1280 1780CRERCE 1400CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	1150 GETGGCATANT  1290 JETTGAGGANI TOTTGAGGANI TOTTGAGAGANI TOT	11700 11700 11700 11700 1300 1700 1700 1
HPV181.1-U EV181.1-U EV181	1041 166CRI 1171 171CTT 1301 156CRG 156CRG 1431 166ATRI GGATRI GGATRI 156TRG 157TRG 15	1050  2016161616  1180  1310  118111111  118111111  1440  1440  1440  1441  14	1060 1060 11190 1190 1320 1320 1450 1450 16TREASTER 16TREASTER 16TREASTER 16TREASTER 16TREASTER 16TREASTER 16TREASTER 16TREASTER 1580 LITEGRATER	1070 CURRETGEC  1200 CURRETGEC  1200 CURRETGEC  1330 INTERCTIF INT	1080 TCTATTGTTE  1210 RTTTRACART  1340 RRCTGCRGAT RRCTGCRGAT 1470 ACCTGTCRGAT 1470 1500 TTCRGCTGCRGAT	1090  1220  ATETOCTIC  1350  GUARANTECT  GUARANTECT  1480  MAGGATECT  1510  ATTECCTCC  ATTECCTCC	1100 1230 REGERTAGE CRETCH CRETCH CRETCH TARTICETER ATRITICETER AT	1110 1240 1240 1240 1240 1240 1240 1240	1120 1250 1250 1250 1250 1250 1250 1250	1130 1260 1260 1260 1260 1260 1260 1260 1360 1360 1380 1380 1380 1520 1520 1571 1671 1671 1671 1671 1671 1671 1671	1140 1270 111496CRGTRATAGER 1270 111496CRGTRATAGER 111486CRGTRATTTRAGERGER 1400 1400 1401 1530 1530 156GRATTGER 1156GRATTGER 1156GRATTG	1150 1280 1780CRERCE 1400CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	1150 GETGGCRITANI 1290 ITGTTGGGGRIT 11GTTGGGGRIT 1420 CERRETRETRETRETRETRETRETRETRETRETRETRETRE	11700 11700 11700 11700 1300 1700 1700 1

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Fig. 6

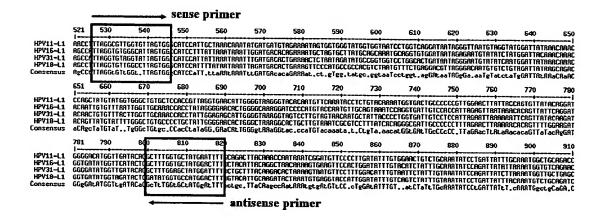
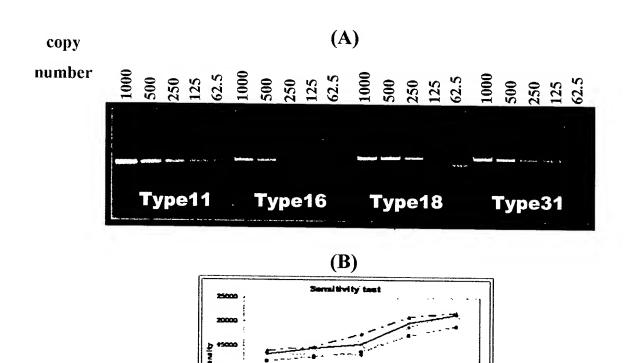


Fig. 7



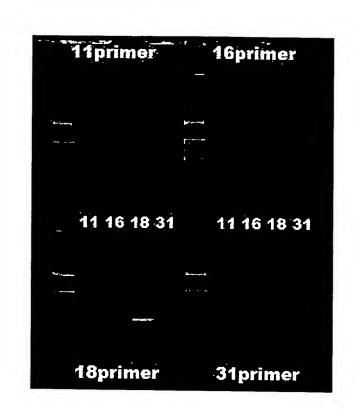
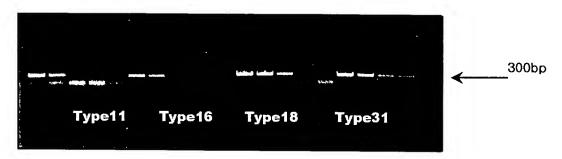
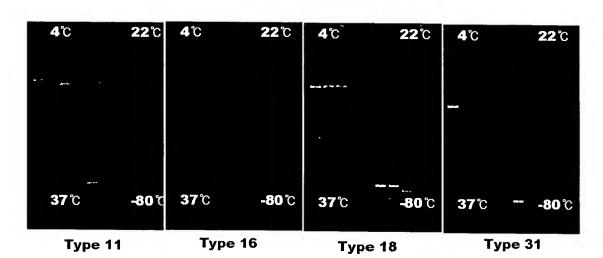


Fig. 9

#### a. Time point : 0 week

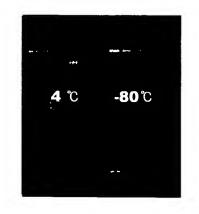


#### b. Time point: 3 week



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Fig. 10



Type11:4 ℃ & -80℃

Y=3.2082X +7596.062 R=0.95

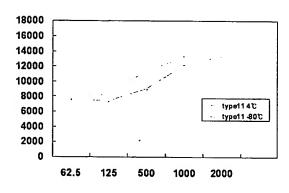
Y=4.219X +8242.484 R=0.97 Type16:4 ℃ & -80 ℃

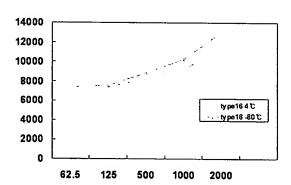
Y=1.888X +7370.587 R=0.99

Y=2.926X +7273.275

R=0.99

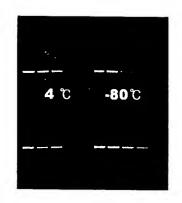
Type11 & Type16





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Fig. 11



Type18:4 ℃ & -80℃

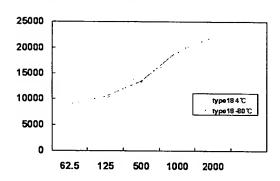
Y=5.705X +10164.36 R=0.95

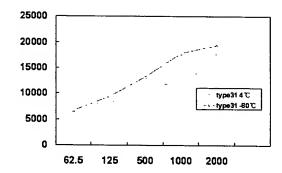
Y=6.7899X +9894.448 R=0.97 Type31:4 ℃ & -80℃

Y=4.6447X +8066.789 R=0.94

Y=6.187X + 8781.618 R=0.92

Type18 & Type31





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Fig. 12

